

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TPRVF 5							
Db	104	TPRVF 108							
RESULT 3									
T12140	Legumin - fava bean (fragment)								
C;Species: Vicia faba (fava bean)									
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004									
C;Accession: T12140									
A;Status: Preliminary; translated from GB/EMBL/DBJ									
A;Residues: 1-136 <HEI>									
A;Cross-references: UNIPROT:Q43672; EMBL:226487; NID:9403333; PMID:8003694									
A;Gene: LeB161									
A;Note: intron positions not resolved (incomplete sequence)									
C;Superfamily: Glycinin									
C;Keywords: seed; storage protein									
RESULT 4									
E69415	Conserved hypothetical protein AF1326 - Archaeoglobus fulgidus								
C;Species: Archaeoglobus fulgidus									
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004									
C;Accession: B69415									
R;Klenk, H. P.; Clayton, R. A.; Tomb, J. F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.									
Nature 390, 364-370, 1997									
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.									
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Archaeoglobus fulgidus									
A;Reference number: A69250; MUID:9809343; PMID:9389475									
A;Accession: E69415									
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown									
A;Molecule type: DNA									
A;Residues: 1-197 <KL>									
A;Cross-references: UNIPROT:Q28943; GB:AE001012; GB:AE000782; NID:92689335; PIDN:ABB8991									
C;Superfamily: hypothetical protein MJ0320; translation elongation factor Tu homology									
C;Keywords: GTP binding; nucleotide binding; P-loop									
F;10-17/Region: nucleotide-binding motif A (P-loop)									
F;132-139/Region: GTP-binding NCKD motif									
F;174-176/Region: GTP-binding SAK/L motif									
RESULT 5									
Qy	1	TPRVF 5							
Db	124	TPRVF 128							

Query Match Score 27; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Accession: S07577
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-339 <HEI>
 A;Cross-references: UNIPROT:PI16079; EMBL:X14240; PIDN:CAA32456.1; PID:929584

Qy 1 TPRVF 5
 Db 145 TPRVF 149

RESULT 8
 JA0152
 Glycinin chain A7 - soybean
 N:Alternate names: seed storage protein
 C:Species: Glycin max (soybean)
 C:Accession: JA0152
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Feb-1995
 R:Kagawa, H.; Hirano, H.
 Plant Sci. 56: 189-195, 1988
 A:Title: Identification and structural characterization of the glycinin seed storage protein
 A:Reference number: JA0152
 A:Accession: JA0152
 A:Molecule type: protein
 A:Residues: 1-212 <KAG>
 A:Experimental source: seed
 C:Comment: Glycinin is the most abundant protein in the soybean seeds. A7 chain is one of the major seed storage proteins.
 C:Superfamily: Glycinin
 Query Match Score 27; DB 2; Length 212;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Accession: S07578
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-335 <HEI>
 A;Cross-references: UNIPROT:PI16080; EMBL:X14241; PIDN:922024; PID:929581

Qy 1 TPRVF 5
 Db 63 TPRVF 67

RESULT 9
 JC2097
 Legumin type B alpha chain precursor (clone LeB4, B4) - tick bean
 C:Species: Vicia faba var. minor (tick bean)
 C:Accession: JC2097
 R:Horstmann, C.; Schlesier, B.; Otto, A.; Kostka, S.; Muentz, K.
 Theor. Appl. Genet. 86: 867-874, 1993
 A:Title: Polymorphism of legumin subunits from field bean (Vicia faba L. var. minor) and tick bean
 A:Reference number: JC2094
 A:Molecule type: DNA
 A:Residues: 1-290 <HOR>
 C:Superfamily: Glycinin
 C:Keywords: seed; storage protein
 P:1-20/Domain: Signal Sequence #status predicted <SIG>
 P:21-268/Product: legumin type B alpha chain #status predicted <MAT>
 Query Match Score 27; DB 2; Length 290;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Accession: S07577
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-335 <HEI>
 A;Cross-references: UNIPROT:PI16078; EMBL:X14237; PIDN:CAA32454.1; PID:92958

Qy 1 TPRVF 5
 Db 181 TPRVF 185

RESULT 10
 S07577
 Legumin storage protein LeB6 - fava bean (fragment)
 C:Species: Vicia faba (fava bean)
 C:Accession: S07577
 C:Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 R:Heim, U.; Schubert, R.; Baumlein, H.; Wobus, U.
 Plant Mol. Biol. 13, 653-663, 1989
 A:Title: The legumin gene family: structure and evolutionary implications of Vicia faba
 A:Reference number: S07576; MUID:91370849; PMID:2491681

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TPRVF 5
 Db 32 TPRVF 36

RESULT 13
 DB3232 Hypothetical protein PA3313 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: DB3232
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Biedrzycki, S.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, R.; Lim, J.; Lory, S.; Olson, M.V.
 N:469 959-964. 2000
 R:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 R:Reference number: A82950; MUID:20437337; PMID:10984043
 R:Accession: DB3232
 R:Status: Preliminary
 A:Residues: 1-335 <STO>
 A:Cross-references: UNIPROT:Q9HHT1; GB:AE004753; GB:AE004091; NID:99949433; PIDN:AG0670
 A:Experimental source: strain PA01
 A:Genes: PA3313

Query Match 100.0%; Score 27; DB 2; Length 335;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TPRVF 5
 Db 37 TPRVF 41

RESULT 14
 T32209 hypothetical protein T0D3.2 - *Ceenorhabditis elegans*
 C:Species: *Ceenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T32209
 R:Murray, J.; Wohldmann, P.; Bauer, C.; Biewald, T.
 Submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of *C. elegans* cosmid T0D3.
 A:Reference number: Z21136
 A:Accession: T32209
 A:Status: Preliminary; translated from GB/EMBL/DDBJ
 A:Residues: 1-335 <MUR>
 A:Cross-references: UNIPROT:O16991; EMBL:AF022380; PIDN:AAB69919.1; GSPDB:GN00023; CESP: S00337
 A:Experimental source: strain Bristol N2; clone T0303
 A:Gene: CESP:T03D3.2
 A:Map position: 5
 A:Introns: 63/3; 186/3; 220/3; 277/2

Query Match 100.0%; Score 27; DB 2; Length 335;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TPRVF 5
 Db 10 TPRVF 14

RESULT 15
 S00337 legumin B Legk precursor - garden pea (fragment)
 N:Alternate names: minor legumin legk
 C:Species: P-sum sativum (garden pea)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004